

## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/731,419A  
Source: FWO  
Date Processed by STIC: 4-20-05

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - cPAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER

10/731,419A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH-ALPHA-1 HEADERS WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleics The number at the end of each line "wrapped" down to the next line. This may occur if your file was received in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 Misaligned Amino Numbering The numbering under each 5' amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 Non-ASCII The submitted file was not saved in ASCII(DOS) text as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)  
(1) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)  
(11) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped

Please also adjust the "(11) NUMBER OF SEQUENCES" response to include the skipped sequences.

8 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  
<210> sequence id number  
<400> sequence id number  
000

9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <211> Response Per 1.823 of Sequence Rules, the only valid <211> responses are Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <211> response is Unknown.

11 Use of <220> Sequence(s) missing the <220> feature and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <211> "Organism" response is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (See 1.823 of Sequence Rules)

12 PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid.

AMC - Biotechnology Systems Branch - 07/07/2003

BEST AVAILABLE COPY



IFWO

## RAW SEQUENCE LISTING

DATE: 04/20/2005

PATENT APPLICATION: US/10/731,419A

TIME: 08:30:17

Input Set : N:\Rasheed\PTO.SR.txt

Output Set: N:\CRF4\04202005\J731419A.raw

3 <110> APPLICANT: Bejjani, Bassem A  
 4 Christensen, Todd M  
 6 <120> TITLE OF INVENTION: Methods of Designing, Synthesizing, and Propagating  
 Reference

7 Nucleic Acids  
 9 <130> FILE REFERENCE: SH1-0001US  
 11 <140> CURRENT APPLICATION NUMBER: US 10/731,419A  
 12 <141> CURRENT FILING DATE: 2003-12-09  
 14 <160> NUMBER OF SEQ ID NOS: 18  
 16 <170> SOFTWARE: PatentIn version 3.3  
 18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 25  
 20 <212> TYPE: DNA  
 21 <213> ORGANISM: Artificial Sequence  
 23 <220> FEATURE:  
 24 <223> OTHER INFORMATION: Arbitrary Example Sequence of Reference Nucleic Acid for  
 Clinical

Does Not Comply  
 Corrected Diskette Needed  
 (pg. 1-24) ←

25 Reference  
 27 <400> SEQUENCE: 1  
 28 agctattcgc tagccgaaat agcgg 25  
 31 <210> SEQ ID NO: 2  
 32 <211> LENGTH: 16  
 33 <212> TYPE: DNA  
 34 <213> ORGANISM: Artificial Sequence  
 36 <220> FEATURE:  
 37 <223> OTHER INFORMATION: Example Synthetic Sequence  
 39 <400> SEQUENCE: 2  
 40 ctggccgctcg ttttac 16  
 43 <210> SEQ ID NO: 3  
 44 <211> LENGTH: 17  
 45 <212> TYPE: DNA  
 46 <213> ORGANISM: Artificial Sequence  
 48 <220> FEATURE:  
 49 <223> OTHER INFORMATION: Example Synthetic Sequence  
 51 <400> SEQUENCE: 3  
 52 caggaaacag ctatgac  
 55 <210> SEQ ID NO: 4  
 56 <211> LENGTH: 16  
 57 <212> TYPE: DNA  
 58 <213> ORGANISM: Example Universal M13 Forward Primer  
 60 <400> SEQUENCE: 4  
 61 gaccggcagc aaaatg  
 64 <210> SEQ ID NO: 5  
 65 <211> LENGTH: 17

pls see item #10  
 on error summary  
 sheet.  
 INVALID  
 response

Mandatory, <213> responses  
 has to be either, Artificial/  
 Unknown or Genus/Species.  
 4/20/05

66 <212> TYPE: DNA

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67 <213> ORGANISM: Example Universal M13 Reverse Primer

69 <400> SEQUENCE: 5

70 caggaaacag ctatgac

73 <210> SEQ ID NO: 6

74 <211> LENGTH: 42

75 <212> TYPE: DNA

76 <213> ORGANISM: Artificial Sequence

78 <220> FEATURE:

79 <223> OTHER INFORMATION: Example Complementary Sequence

81 <400> SEQUENCE: 6

82 gtcctttgtc gatactgtcg ataagcgatc ggctttatcg cc

42

85 <210> SEQ ID NO: 7

86 <211> LENGTH: 41

87 <212> TYPE: DNA

88 <213> ORGANISM: Artificial Sequence

90 <220> FEATURE:

91 <223> OTHER INFORMATION: Example Strand from Duplex Synthesis

93 <400> SEQUENCE: 7

94 tcgataagcg atcggtttta tcgccgaccg gcagcaaaat g

41

97 <210> SEQ ID NO: 8

98 <211> LENGTH: 17

99 <212> TYPE: DNA

100 <213> ORGANISM: Artificial Sequence

102 <220> FEATURE:

103 <223> OTHER INFORMATION: Example Synthetic Tag Sequence

105 <400> SEQUENCE: 8

106 gtcctttgtc gatactg

17

109 <210> SEQ ID NO: 9

110 <211> LENGTH: 37

111 <212> TYPE: DNA

112 <213> ORGANISM: Artificial Sequence

114 <220> FEATURE:

115 <223> OTHER INFORMATION: Example Second Strand from Duplex Synthesis

117 <400> SEQUENCE: 9

118 caggaaacag ctatgacagc tattcgctag ccgaaat

37

121 <210> SEQ ID NO: 10

122 <211> LENGTH: 9

123 <212> TYPE: DNA

124 <213> ORGANISM: Artificial Sequence

126 <220> FEATURE:

127 <223> OTHER INFORMATION: Example Synthetic First Tag

129 <400> SEQUENCE: 10

130 tgatgatga

9

133 <210> SEQ ID NO: 11

134 <211> LENGTH: 8

135 <212> TYPE: DNA

136 <213> ORGANISM: Artificial Sequence

138 <220> FEATURE:

139 <223> OTHER INFORMATION: Example Synthetic Second Tag

Invalid  
response

17  
pls see item #10 on  
error summary  
sheet,

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TIME: 08:30:17

Input Set : N:\Rasheed\PTO.SR.txt

Output Set: N:\CRF4\04202005\J731419A.raw

141 <400> SEQUENCE: 11  
142 ccggaatt 8  
145 <210> SEQ ID NO: 12  
146 <211> LENGTH: 13  
147 <212> TYPE: DNA  
148 <213> ORGANISM: Artificial Sequence  
150 <220> FEATURE:  
151 <223> OTHER INFORMATION: Example First Oligonucleotide  
153 <400> SEQUENCE: 12  
154 agattcgcta gcc 13  
157 <210> SEQ ID NO: 13  
158 <211> LENGTH: 13  
159 <212> TYPE: DNA  
160 <213> ORGANISM: Artificial Sequence  
162 <220> FEATURE:  
163 <223> OTHER INFORMATION: Example Second Oligonucleotide  
165 <400> SEQUENCE: 13  
166 gaaatcgtag cgg 13  
169 <210> SEQ ID NO: 14  
170 <211> LENGTH: 12  
171 <212> TYPE: DNA  
172 <213> ORGANISM: Artificial Sequence  
174 <220> FEATURE:  
175 <223> OTHER INFORMATION: Example Complement Bridge Sequence  
177 <400> SEQUENCE: 14  
178 gatcggttt ag  
181 <210> SEQ ID NO: 15  
182 <211> LENGTH: 26  
183 <212> TYPE: DNA  
184 <213> ORGANISM: Artificial Sequence  
186 <220> FEATURE:  
187 <223> OTHER INFORMATION: Example Ligation Sequence  
189 <400> SEQUENCE: 15  
190 agattcgcta gccgaaatcg tagcgg 26  
193 <210> SEQ ID NO: 16  
194 <211> LENGTH: 6  
195 <212> TYPE: DNA  
196 <213> ORGANISM: Artificial Sequence  
198 <220> FEATURE:  
199 <223> OTHER INFORMATION: Example Synthetic Overlap Extension Complementary Strand End  
201 <400> SEQUENCE: 16  
202 ctttag 6  
205 <210> SEQ ID NO: 17  
206 <211> LENGTH: 59  
207 <212> TYPE: DNA  
208 <213> ORGANISM: Artificial Sequence  
210 <220> FEATURE:  
211 <223> OTHER INFORMATION: Example Strand Sequence from Overlap Extension Method  
213 <400> SEQUENCE: 17

← What is the source of genetic material?

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Input Set : N:\Rasheed\PTO.SR.txt

Output Set: N:\CRF4\04202005\J731419A.raw

```
214 gtcctttgtc gatactgaga ttcgctagcc ctttagcatc gccgaccggc agcaaaatg      59
217 <210> SEQ ID NO: 18
218 <211> LENGTH: 59
219 <212> TYPE: DNA
220 <213> ORGANISM: Artificial Sequence
222 <220> FEATURE:
223 <223> OTHER INFORMATION: Example Second Strand Sequence from Overlap Extension Method
225 <400> SEQUENCE: 18
226 caggaaacag ctatgactct aagcgatcgg gaaatcgtag cggctggccg tcgttttac      59
```

**VERIFICATION SUMMARY**

DATE: 04/20/2005

PATENT APPLICATION: US/10/731,419A

TIME: 08:30:18

Input Set : N:\Rasheed\PTO.SR.txt

Output Set: N:\CRF4\04202005\J731419A.raw